

10/018094

JC Rec'd PCT/PTO 14 DEC 2001

(Nucleotide) FASTA of: Hn540-1.Dna from: 1 to: 3705 September 25, 19100 23:27

REFORMAT of: Hn540-1.Dna check: 5366 from: 1 to: 3705 September 25, 19100
13:37

(No documentation)

TO: @USER_DISK:[Z8SE007]134608.\$TMP Sequences: 7,218,604 Symbols: -151,773,6
69 Word Size: 6

Sequences too short to analyze: 62 (231 symbols)

Databases searched:

EMBL, Release 63.0, Released on 10Jun2000, Formatted on 10Jul2000

EMBL, Release 63.0, Released on 17Jun2000, Formatted on 17Jul2000

EMBL, Release 63.0, Released on 25Jun2000, Formatted on 25Jul2000

EMBL, Release 63.0, Released on 6Jun2000, Formatted on 6Jul2000

EMBL, Release 63.0, Released on 14Jun2000, Formatted on 14Jul2000

EMBL, Release 63.0, Released on 19Jun2000, Formatted on 19Jul2000

EMBL, Release 63.0, Released on 20Jun2000, Formatted on 20Jul2000

EMBL, Release 63.0, Released on 11Jun2000, Formatted on 11Jul2000

EMBL, Release 63.0, Released on 18Jun2000, Formatted on 18Jul2000

GeneSeq, Release 40.4, Released on 22Jun2000, Formatted on 22Jun2000

EMBL, Release 63.0, Released on 3Jun2000, Formatted on 3Jul2000

EMBL, Release 63.0, Released on 4Jun2000, Formatted on 4Jul2000

EMBL, Release 63.0, Released on 5Jun2000, Formatted on 5Jul2000

EMBL, Release 63.0, Released on 7Jun2000, Formatted on 7Jul2000

Searching with both strands of the query.

Scoring matrix: GenRunData:Fastadna.Cmp

Constant pamfactor used

Gap creation penalty: 16 Gap extension penalty: 4

Results sorted a z-values calculated from initial score
1673 scores saved that exceeded 116, Joining threshold: 91, opt. width: 16

The best scores are: init1 initn opt z-sc E(14420799)...

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Emrod:Af125521   Begin: 1   End: 3705
! Af125521 Rattus norvegicus nephrin ...18525 18525 18525 25999.4      0
Emrod:Af161715   Begin: 458   End: 4162
! Af161715 Rattus norvegicus nephrin ...18452 18452 18453 25893.3      0
Emrod:Af168466   Begin: 24   End: 3481

! Af168466 Mus musculus nephrin (Nphs...14308 15239 14974 21379.6      0
Emhum1:Af035835   Begin: 24   End: 3497
! Af035835 Homo sapiens nephrin (NPHS...11557 12214 12066 17125.7      0
Gcg_Geneseq_D:Z25338   Begin: 24   End: 3497
! Human nephrin nucleotide sequence. ...11557 12214 12066 17125.7      0
Emhum3:Hsac2133   Begin: 14708   End: 14893   Strand: -
! Ac002133 Human DNA from chromosome ... 651 4463 651 6211.3      0
Emhtg5:Ac022315   Begin: 169005   End: 169234
! Ac022315 Homo sapiens chromosome N/... 653 2207 700 3028.6      0
Emhum6:Hsu95090   Begin: 33243   End: 33369   Strand: -
! U95090 Homo sapiens chromosome 19 c... 448 1773 455 2430.1      0

Emest_Mam:Aw347107   Begin: 1   End: 426
! Aw347107 30251 MARC 1PIG Sus scrofa... 1431 1431 1437 1983.9      0
Emgss6:Aq522774   Begin: 252   End: 437
! Aq522774 HS_5221_B1_E10_T7A RPCI-11... 586 956 603 1314.0      0
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Hn540-1.Dna

Emrod:Af125521

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ID   AF125521   standard; RNA; ROD; 3705 BP.
AC   AF125521;
SV   AF125521.1
DT   23-NOV-1999 (Rel. 61, Created)
DT   23-NOV-1999 (Rel. 61, Last updated, Version 1)
DE   Rattus norvegicus nephrin mRNA, complete cds.
KW   .
OS   Rattus norvegicus (Norway rat)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN   [1]
RP   1-3705
RX   MEDLINE; 99419288.
RA   Ahola H., Wang S.X., Luimula P., Solin M.L., Holzman L.B., Holthofer H.;
RT   "Cloning and expression of the rat nephrin homolog";
RL   Am. J. Pathol. 155(3):907-913(1999).
RN   [2]
RP   1-3705
RA   Ahola H., Wang S.-X., Luimula P., Solin M.-L., Holzman L.B., Holthofer H.;
RT   ;
RL   Submitted (03-FEB-1999) to the EMBL/GenBank/DDBJ databases.
RL   Haartman Institute/ Division of Bacteriology and Immunology, University of
RL   Helsinki, P.O. Box 21 (Haartmaninkatu 3), Helsinki 00014, Finland
DR   SPTREMBL; Q9R044; Q9R044.
FH   Key          Location/Qualifiers
FH
FT   source          1. .3705

FT          /db_xref="taxon:10116"
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FT          /strain="Sprague-Dawley"
FT          /tissue_type="kidney glomeruli"
FT          /dev_stage="one month"
FT   CDS          1. .3705
FT          /codon_start=1
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FT      /protein_id="AAF12734.1"
FT      /translation="MSSLTPLLMLTSGLAESPVPTSAPRGFWALSENLTAVEGTTV
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FT
FT      YECQVGRSELGPPELVSPKVIILSVSPKVLTLTPEAGSTVTWVAGQEYVVTCVSGDAKP
FT
FT      APDITFIQSGRTILDVSSNVNEGSEEKLCITEAEARVIPQSSDNGQLLVCEGSNPALDT
FT
FT      PIKASFTMNILFPPGPPVIDWPGLNEGHRAGENLELPCTARGGNPPATLQWLKNGKPV
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FT      STAWGTEHAQAVAHSVLVMTVRPEDHGARLSCQSYNSVSAGTQERSITLQVTFPPSAIT
FT
FT      ILGSVSQSENKNVTLCCLTKSSRPVLLRWLWLGGRQLLPTDETVM DGLHGGHISMSNLT
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FT      FLVRREDNGLPLTCEAFSDAFSKETFKKSLTLNVKYPQKWLWIEGPPEGQYIRTGTRVR
FT
FT      LVCLAIGGNPDPSLIWFKDSRPVSEPRQPQEP RRVLGSGVEKSGSTFSRELVLII GPPD
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FT      NRAKFSCKAGQLSASTQLVVQFPPTNLTI LANSSALRPGDALNLTCVSISSNPPVNL SW
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SCORES Init1: 18525 Initn: 18525 Opt: 18525 z-score: 25999.4 E(): 0
100.0% identity in 3705 bp overlap

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Af125521	ATGTCCAGTTTGACTCCCCTGCTGCTCATGGGAATGCTGACCTCAGGCCTGGCCGAGTCG					
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	70	80	90	100	110	120
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Af125521	CCAGTCCCCACCTCAGCACCTCGAGGCTTCTGGGCTCTGTCTGAAAACCTGACTGCGGTG					
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	130	140	150	160	170	180
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Af125521	GAAGGGACAACAGTTAAGCTATGGTGCGGTGTCAGGGCCCTGGCAGTGTGGTGCACTGG					
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	190	200	210	220	230	240
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Af125521	GCTAAGGATGGGCTGCTTCTGGGTCCAAACCCGAAGATGCCAGGCTTCCCAGGTACAGC					
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	250	260	270	280	290	300
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Af125521	CTGGAAGGAGATCGTGCTAAAGGCGAGTTCCACCTGCTTATTGAAGCCTGTGACCTCAGT					
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	310	320	330	340	350	360
Hn540-1.Dna	GATGACGCAGAGTATGAATGCCAAGTCGGCCGCTCAGAGTTGGGTCCCAGCTTGTGTCT					

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Af125521  GATGACGCAGAGTATGAATGCCAAGTCGGCCGCTCAGAGTTGGGTCCCAGCTTGTGTCT
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              370      380      390      400      410      420
Hn540-1.Dna CCTAAAGTAATCCTCTCCATTCTAGTTTCCCCCAAGGTGCTTCTGTTGACCCCCGAGGCA

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Af125521  CCTAAAGTAATCCTCTCCATTCTAGTTTCCCCCAAGGTGCTTCTGTTGACCCCCGAGGCA
              370      380      390      400      410      420

              430      440      450      460      470      480
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Af125521  GGAAGCACAGTGACCTGGGTAGCTGGGCAGGAGTATGTGGTCACCTGTGTGTCTGGGGAT
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              490      500      510      520      530      540
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Af125521  GCAAAAACCAGCACCTGACATCACCTTCATCCAGAGTGGACGAACTATATTGGACGTCTCC
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              610      620      630      640      650      660

              670      680      690      700      710      720
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Af125521  ATTGATTGGCCAGGCCTGAATGAAGGGCATGTGAGGGCAGGGGAGAACCTGGAGCTGCCC
              730      740      750      760      770      780

              790      800      810      820      830      840
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Af125521  TGCACAGCCAGAGGTGGCAATCCACCTGCTACCCTGCAGTGGCTGAAGAACGGTAAACCA
              790      800      810      820      830      840

              850      860      870      880      890      900
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Af125521  GTGTCCACAGCCTGGGGCACCAGCATGCCAGGCAGTGGCCCACAGTGTGCTGGTGATG
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              910      920      930      940      950      960
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		1030	1040	1050	1060	1070	1080
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Af125521	ATCCTGGGATCTGTATCACAATCGGAGAACAAGAACGTGACCCTTTGCTGCCTGACCAAG						
		1030	1040	1050	1060	1070	1080
		1090	1100	1110	1120	1130	1140
Hn540-1.Dna	TCCAGTCGCCCACGGGTCCTGCTGCGATGGTGGTTGGGTGGACGGCAGCTGCTGCCCACA						
Af125521	TCCAGTCGCCCACGGGTCCTGCTGCGATGGTGGTTGGGTGGACGGCAGCTGCTGCCCACA						
		1090	1100	1110	1120	1130	1140
		1150	1160	1170	1180	1190	1200
Hn540-1.Dna	GATGAGACAGTCATGGATGGCCTGCATGGTGGCCACATCTCCATGTCCAATCTCACATTC						
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		1210	1220	1230	1240	1250	1260
Hn540-1.Dna	TTGGTGCGGAGAGAAGACAATGGCCTGCCCTCACGTGTGAAGCCTTCAGTGACGCCTTC						
Af125521	TTGGTGCGGAGAGAAGACAATGGCCTGCCCTCACGTGTGAAGCCTTCAGTGACGCCTTC						
		1210	1220	1230	1240	1250	1260
		1270	1280	1290	1300	1310	1320
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Af125521	AGCAAGGAGACCTTCAAGAAGTCACTCACCTTGAATGTGAAATACCCTGCCCAGAAGCTG						
		1270	1280	1290	1300	1310	1320
		1330	1340	1350	1360	1370	1380
Hn540-1.Dna	TGGATTGAGGGGCCCCCAGAGGGACAGTACATCCGGACTGGGACTCGGGTGAGGCTGGTA						
Af125521	TGGATTGAGGGGCCCCCAGAGGGACAGTACATCCGGACTGGGACTCGGGTGAGGCTGGTA						
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		1390	1400	1410	1420	1430	1440
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Af125521	TGCTTGGCCATCGGAGGCAACCCAGACCCCTCCCTCATCTGGTTTAAGGATTACGTC						
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		1450	1460	1470	1480	1490	1500
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Af125521	GTGAGCGAGCCCCGGCAGCCCCAGGAGCCCCGGCGTGTGCAGCTGGGCAGTGTGGAGAAG						
		1450	1460	1470	1480	1490	1500
		1510	1520	1530	1540	1550	1560
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		1510	1520	1530	1540	1550	1560
		1570	1580	1590	1600	1610	1620
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Af125521 AAGTTCCTCGCAAGGCGGGTCAGCTCAGTGCCTCTAGCCAGCTGGTGGTGCAGTTCCCC
1570 1580 1590 1600 1610 1620

Hn540-1.Dna 1630 1640 1650 1660 1670 1680
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1870 1880 1890 1900 1910 1920

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1930 1940 1950 1960 1970 1980

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Af125521 GGCTACCGCCTCAGCCCAGCTGGGGGTCCCCGGCACCGTATCCTGTCTGGAGGGGCTCTG
2050 2060 2070 2080 2090 2100

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	2290	2300	2310	2320	2330	2340
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	2350	2360	2370	2380	2390	2400
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	2410	2420	2430	2440	2450	2460
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	2410	2420	2430	2440	2450	2460
	2470	2480	2490	2500	2510	2520
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Af125521	GCAGCCAGAGGACTGGTTCGTCTTGTTCGTCCGATTTGCTCCCCAGGTGGATCAGCCTACT					
	2470	2480	2490	2500	2510	2520
	2530	2540	2550	2560	2570	2580
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Af125521	CCCCTAACAAAAGTGGCTGCCGCTGGGGACAGCACCAGCTCAGCCACACTGCACTGCCGT					
	2530	2540	2550	2560	2570	2580
	2590	2600	2610	2620	2630	2640
Hn540-1.Dna	GCCCCGGGTGTCCCCAACATCGACTTCACTTGGACCAAAAACGGGGTCCCTCTGGATCTC					
Af125521	GCCCCGGGTGTCCCCAACATCGACTTCACTTGGACCAAAAACGGGGTCCCTCTGGATCTC					
	2590	2600	2610	2620	2630	2640
	2650	2660	2670	2680	2690	2700
Hn540-1.Dna	CAAGACCCCAGGTACACAGAGCACAGGTACCACCAGGGTGTGTCCACAGCAGCCTCTTG					
Af125521	CAAGACCCCAGGTACACAGAGCACAGGTACCACCAGGGTGTGTCCACAGCAGCCTCTTG					
	2650	2660	2670	2680	2690	2700
	2710	2720	2730	2740	2750	2760
Hn540-1.Dna	ACCATCGCTAATGTGTCTGCGGCCAGGACTATGCCCTCTTCAAATGCACGGCCACCAAT					
Af125521	ACCATCGCTAATGTGTCTGCGGCCAGGACTATGCCCTCTTCAAATGCACGGCCACCAAT					
	2710	2720	2730	2740	2750	2760
	2770	2780	2790	2800	2810	2820
Hn540-1.Dna	GCCCTTGGCTCTGACCACACCAACATCCAGCTCGTCAGCATCAGCCGCCCTGACCCTCCA					
Af125521	GCCCTTGGCTCTGACCACACCAACATCCAGCTCGTCAGCATCAGCCGCCCTGACCCTCCA					
	2770	2780	2790	2800	2810	2820
	2830	2840	2850	2860	2870	2880
Hn540-1.Dna	CTGGGACTGAAGGTTGTCAGCATAAGCCCTCACTCGGTGGGGCTGGAGTGAAGCCTGGC					
Af125521	CTGGGACTGAAGGTTGTCAGCATAAGCCCTCACTCGGTGGGGCTGGAGTGAAGCCTGGC					

	2830	2840	2850	2860	2870	2880
	2890	2900	2910	2920	2930	2940
Hn540-1.Dna	TTTGATGGGGGTCTGCCTCAGAGGTTCCAAATCAGGTACGAGGCCCTCGAGACCCCAGGA					
Af125521	TTTGATGGGGGTCTGCCTCAGAGGTTCCAAATCAGGTACGAGGCCCTCGAGACCCCAGGA					
	2890	2900	2910	2920	2930	2940
	2950	2960	2970	2980	2990	3000
Hn540-1.Dna	TTCCTCCACGTGGATGTCCTACCTACACAGGCCACTACCTTCACGCTGACTGGGCTGAAG					
Af125521	TTCCTCCACGTGGATGTCCTACCTACACAGGCCACTACCTTCACGCTGACTGGGCTGAAG					
	2950	2960	2970	2980	2990	3000
	3010	3020	3030	3040	3050	3060
Hn540-1.Dna	CCTTCTACACGATATAGGATCTGGCTGTTGGCCAGCAATGCCCTGGGGGACAGTGGATTG					
Af125521	CCTTCTACACGATATAGGATCTGGCTGTTGGCCAGCAATGCCCTGGGGGACAGTGGATTG					
	3010	3020	3030	3040	3050	3060
	3070	3080	3090	3100	3110	3120
Hn540-1.Dna	ACGGACAAGGGGATCCAGGTCTCCGTCACTACCCCAGGCCCGACCAGGCTCCTGAAGAC					
Af125521	ACGGACAAGGGGATCCAGGTCTCCGTCACTACCCCAGGCCCGACCAGGCTCCTGAAGAC					
	3070	3080	3090	3100	3110	3120
	3130	3140	3150	3160	3170	3180
Hn540-1.Dna	ACAGACCACCAGCTGCCCACAGAGCTGCCTCCAGGACCCCCAAGGCTGCCCCTGCTGCCT					
Af125521	ACAGACCACCAGCTGCCCACAGAGCTGCCTCCAGGACCCCCAAGGCTGCCCCTGCTGCCT					
	3130	3140	3150	3160	3170	3180
	3190	3200	3210	3220	3230	3240
Hn540-1.Dna	GTGCTCTTTGCAGTTGGTGGTCTTCTGCTGCTCTCCAATGCCTCCTGTGTTGGGGGTCTC					
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	3190	3200	3210	3220	3230	3240
	3250	3260	3270	3280	3290	3300
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Af125521	CTCTGGCGGAGAAGACTGAGGCGCCTTGCTGAGGAGATCTCAGAGAAGACAGAGGCAGGG					
	3250	3260	3270	3280	3290	3300
	3310	3320	3330	3340	3350	3360
Hn540-1.Dna	TCGGAGGACAGGATCAGGAATGAATATGAGGAGAGTCAGTGGACTGGGGACCGGGACACG					
Af125521	TCGGAGGACAGGATCAGGAATGAATATGAGGAGAGTCAGTGGACTGGGGACCGGGACACG					
	3310	3320	3330	3340	3350	3360
	3370	3380	3390	3400	3410	3420
Hn540-1.Dna	AGAAGCTCCACGGTTAGCACAGCAGAAGTGGACCCAAATTACTACTCCATGAGGGACTTC					
Af125521	AGAAGCTCCACGGTTAGCACAGCAGAAGTGGACCCAAATTACTACTCCATGAGGGACTTC					
	3370	3380	3390	3400	3410	3420
	3430	3440	3450	3460	3470	3480
Hn540-1.Dna	AGCCCCAGCTTCCCCCAACACTGGAGGAGGTGCTGTATCACCAAGGTGCTGAAGGCGAG					
Af125521	AGCCCCAGCTTCCCCCAACACTGGAGGAGGTGCTGTATCACCAAGGTGCTGAAGGCGAG					
	3430	3440	3450	3460	3470	3480
	3490	3500	3510	3520	3530	3540
Hn540-1.Dna	GACATGGCCTTCCCCGGACACCTGCATGATGAAGTGGAGAGAGCCTATGGCCCCGCTGGG					


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Af125521      GACATGGCCTTCCCCGGACACCTGCATGATGAAGTGGAGAGAGCCTATGGCCCGCCTGGG
                3490      3500      3510      3520      3530      3540
                3550      3560      3570      3580      3590      3600
Hn540-1.Dna   GCCTGGGGACCCCTCTATGATGAAGTACGAATGGACCCCTATGACCTTCGCTGGCCTGAG
                |||||
Af125521      GCCTGGGGACCCCTCTATGATGAAGTACGAATGGACCCCTATGACCTTCGCTGGCCTGAG
                3550      3560      3570      3580      3590      3600
                3610      3620      3630      3640      3650      3660
Hn540-1.Dna   GTCCAATGTGAGGATCCGAGGGGAATCTACAACCAGGTGGCAGCAGACATGGATGCTGTG
                |||||
Af125521      GTCCAATGTGAGGATCCGAGGGGAATCTACAACCAGGTGGCAGCAGACATGGATGCTGTG
                3610      3620      3630      3640      3650      3660
                3670      3680      3690      3700
Hn540-1.Dna   GAAGCTAGCTCTCTGCCGTTTGTAGCTGAGGGGACATCTGGTGTGA
                |||||
Af125521      GAAGCTAGCTCTCTGCCGTTTGTAGCTGAGGGGACATCTGGTGTGA
                3670      3680      3690      3700

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Hn540-1.Dna
Emrod:Af161715

ID AF161715 standard; RNA; ROD; 5820 BP.
AC AF161715;
SV AF161715.1
DT 12-DEC-1999 (Rel. 62, Created)

DT 12-DEC-1999 (Rel. 62, Last updated, Version 1)
DE Rattus norvegicus nephrin mRNA, complete cds.
KW .
OS Rattus norvegicus (Norway rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]
RP 1-5820
RA Kawachi H., Koike H., Yaoita E., Yamamoto T., Orikasa M., Shimizu F.;
RT "Cloning of rat nephrin and its expression and localization in proteinuric
RT states";
RL Unpublished.
RN [2]
RP 1-5820
RA Kawachi H., Koike H., Yaoita E., Yamamoto T., Orikasa M., Shimizu F.;
RT ;
RL Submitted (22-JUN-1999) to the EMBL/GenBank/DDBJ databases.

RL Department of Cell Biology, Institute of Nephrology, Niigata University
RL School of Medicine, 1-757 Asahimachi-dori, Niigata 951-8510, Japan
DR SPTREMBL; Q9QXX7; Q9QXX7.

FH Key Location/Qualifiers

FH
FT source 1. 5820
FT /db_xref="taxon:10116"
FT /organism="Rattus norvegicus"
FT /strain="Wistar"
FT /tissue_type="glomeruli"
FT CDS 404. 4162
FT /codon_start=1
FT /db_xref="SPTREMBL:Q9QXX7"
FT /product="nephrin"
FT /protein_id="AAF14884.1"
FT /translation="MGAKRVTVRGARTSPIHRTSSLTPLLMLTSGLAESPVFTSAP

QWAKDGLLLGPNPKMPGFPRYSLEGDR

SCORES Init1: 18452 Initn: 18452 Opt: 18453 z-score: 25893.3 E(): 0
99.8% identity in 3705 bp overlap

Page -12-

	730	740	750	760	770	780
	340	350	360	370	380	390
Hn540-1.Dna	CGCTCAGAGTTGGGTCCCGAGCTTGTGTCTCCTAAAGTAATCCTCTCCATTCTAGTTTCC					
Af161715	CGCTCAGAGTTGGGTCCCGAGCTTGTGTCTCCTAAAGTAATCCTCTCCATTCTAGTTTCC					
	790	800	810	820	830	840
	400	410	420	430	440	450
Hn540-1.Dna	CCCAAGGTGCTTCTGTTGACCCCCGAGGCAGGAAGCACAGTGACCTGGGTAGCTGGGCAG					
Af161715	CCCAAGGTGCTTCTGTTGACCCCCGAGGCAGGAAGCACAGTGACCTGGGTAGCTGGGCAG					
	850	860	870	880	890	900
	460	470	480	490	500	510
Hn540-1.Dna	GAGTATGTGGTCACCTGTGTGTCTGGGGATGCAAAACCAGCACCTGACATCACCTTCATC					
Af161715	GAGTATGTGGTCACCTGTGTGTCTGGAGATGCAAAACCAGCACCTGACATCACCTTCATC					
	910	920	930	940	950	960
	520	530	540	550	560	570
Hn540-1.Dna	CAGAGTGGACGAACTATATTGGACGTCTCCTCCAATGTGAATGAGGGATCAGAGGAGAAA					
Af161715	CAGAGTGGACGAACTATATTGGACGTCTCCTCCAATGTGAATGAGGGATCAGAGGAGAAA					
	970	980	990	1000	1010	1020
	580	590	600	610	620	630
Hn540-1.Dna	CTCTGCATCACAGAGGCCGAAGCCAGGGTGATACCCAGAGCTCGGATAACGGGCAGTTA					
Af161715	CTCTGCATCACAGAGGCCGAAGCCAGGGTGATACCCAGAGCTCGGATAACGGGCAGTTA					
	1030	1040	1050	1060	1070	1080
	640	650	660	670	680	690
Hn540-1.Dna	CTGGTCTGTGAGGGTTCCAACCCAGCTTTGGACACTCCCATAAAGGCTTCATTACCATG					
Af161715	CTGGTCTGTGAGGGTTCCAACCCAGCTTTGGACACTCCCATAAAGGCTTCATTACCATG					
	1090	1100	1110	1120	1130	1140
	700	710	720	730	740	750
Hn540-1.Dna	AATATTCTGTTTCCCCCAGGACCTCCTGTCATTGATTGGCCAGGCCTGAATGAAGGGCAT					
Af161715	AATATTCTGTTTCCCCCAGGACCTCCTGTCATTGATTGGCCAGGCCTGAATGAAGGGCAT					
	1150	1160	1170	1180	1190	1200
	760	770	780	790	800	810
Hn540-1.Dna	GTGAGGGCAGGGGAGAACCTGGAGCTGCCCTGCACAGCCAGAGGTGGCAATCCACCTGCT					
Af161715	GTGAGGGCAGGGGAGAACCTGGAGCTGCCCTGCACAGCCAGAGGTGGCAATCCACCTGCT					
	1210	1220	1230	1240	1250	1260
	820	830	840	850	860	870
Hn540-1.Dna	ACCCTGCAGTGGCTGAAGAACGGTAAACCAGTGTCCACAGCCTGGGGCACCAGCATGCC					
Af161715	ACCCTGCAGTGGCTGAAGAACGGTAAACCAGTGTCCACAGCCTGGGGCACCAGCATGCC					
	1270	1280	1290	1300	1310	1320
	880	890	900	910	920	930
Hn540-1.Dna	CAGGCAGTGGCCACAGTGTGCTGGTGATGACTGTACGACCTGAAGACCATGGAGCTCGG					
Af161715	CAGGCAGTGGCCACAGCGTGTGCTGGTGATGACTGTACGACCTGAAGACCATGGAGCTCGG					
	1330	1340	1350	1360	1370	1380
	940	950	960	970	980	990
Hn540-1.Dna	CTCAGCTGTCAGTCCTACAACAGCGTGTCTGCAGGGACCCAGGAGAGAAGCATCACACTA					

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|||||
Af161715   CTCAGCTGTCAGTCCCTACAACAGCGTGTCTGCAGGGACCCAGGAGAGAAGCATCACACTA
1390       1400       1410       1420       1430       1440

          1000       1010       1020       1030       1040       1050
Hn540-1.Dna CAGGTCACCTTTCCCCCAAGCGCCATTACCATCCTGGGATCTGTATCACAATCGGAGAAC
|||||
Af161715   CAGGTCACCTTTCCCCCAAGCGCCATTACCATCCTGGGATCTGTATCACAATCGGAGAAC
1450       1460       1470       1480       1490       1500

          1060       1070       1080       1090       1100       1110
Hn540-1.Dna AAGAACGTGACCCTTTGCTGCCTGACCAAGTCCAGTCGCCCACGGGTCCTGCTGCGATGG
|||||
Af161715   AAGAACGTGACCCTTTGCTGCCTGACCAAGTCCAGTCGCCCACGGGTCCTGCTGCGATGG
1510       1520       1530       1540       1550       1560

          1120       1130       1140       1150       1160       1170
Hn540-1.Dna TGGTTGGGTGGACGGCAGCTGCTGCCCACAGATGAGACAGTCATGGATGGCCTGCATGGT
|||||
Af161715   TGGTTGGGTGGACGGCAGCTGCTGCCCACAGATGAGACAGTCATGGATGGCCTGCATGGT
1570       1580       1590       1600       1610       1620

          1180       1190       1200       1210       1220       1230
Hn540-1.Dna GGCCACATCTCCATGTCCAATCTCACATTCTTGGTGCGGAGAGAAGACAATGGCCTGCCC
|||||
Af161715   GGCCACATCTCCATGTCCAATCTCACATTCTTGGTGCGGAGAGAAGACAATGGCCTGCCC
1630       1640       1650       1660       1670       1680

          1240       1250       1260       1270       1280       1290
Hn540-1.Dna CTCACGTGTGAAGCCTTCAGTGACGCCTTCAGCAAGGAGACCTTCAAGAAGTCACTCACC
|||||
Af161715   CTCACCTGTGAAGCCTTCAGTGACGCCTTCAGCAAGGAGACCTTCAAGAAGTCACTCACC
1690       1700       1710       1720       1730       1740

          1300       1310       1320       1330       1340       1350
Hn540-1.Dna TTGAATGTGAAATACCCTGCCCAGAAGCTGTGGATTGAGGGGCCCCCAGAGGGACAGTAC
|||||
Af161715   TTGAATGTGAAATACCCTGCCCAGAAGCTGTGGATTGAGGGGCCCCCAGAGGGACAGTAC
1750       1760       1770       1780       1790       1800

          1360       1370       1380       1390       1400       1410
Hn540-1.Dna ATCCGGACTGGGACTCGGGTGAGGCTGGTATGCTTGGCCATCGGAGGCAACCCAGACCCC
|||||
Af161715   ATCCGGACTGGGACTCGGGTGAGGCTGGTATGCTTGGCCATCGGAGGCAACCCAGACCCC
1810       1820       1830       1840       1850       1860

          1420       1430       1440       1450       1460       1470
Hn540-1.Dna TCCCTCATCTGGTTTAAAGATTACGTCGGGTGAGCGAGCCCCGGCAGCCCCAGGAGCCC
|||||
Af161715   TCCCTCATCTGGTTTAAAGATTACGTCGGGTGAGCGAGCCCCGGCAGCCCCAGGAGCCC
1870       1880       1890       1900       1910       1920

          1480       1490       1500       1510       1520       1530
Hn540-1.Dna CGGCGTGTGCAGCTGGGCAGTGTGGAGAAGTCCGGGAGCACTTTCTCCGCGAGCTGGTG
|||||
Af161715   CGGCGTGTGCAGCTGGGCAGTGTGGAGAAGTCCGGGAGCACTTTCTCCGCGAGCTGGTG
1930       1940       1950       1960       1970       1980

          1540       1550       1560       1570       1580       1590
Hn540-1.Dna TTGATCATAGGTCCGCCGGACAACCGAGCCAAGTTCTCCTGCAAGGCGGGTCAGCTCAGT
|||||
Af161715   TTGATCATAGGTCCGCCGGACAACCGAGCCAAGTTCTCCTGCAAGGCGGGTCAGCTCAGT
1990       2000       2010       2020       2030       2040
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1600 1610 1620 1630 1640 1650

Hn540-1.Dna GCGTCTACGCAGCTGGTGGTGCAGTTCCCCCAACCAACCTGACCATCCTGGCCAACTCG
|||||
Af161715 GCGTCTACGCAGCTGGTGGTGCAGTTCCCCCAACCAACCTGACCATCCTGGCCAACTCG
2050 2060 2070 2080 2090 2100

1660 1670 1680 1690 1700 1710

Hn540-1.Dna TCCGCGCTGCGCCAGGCGACGCCTTGAACCTGACCTGCGTCAGCATCAGCAGCAACCCC
|||||
Af161715 TCCGCGCTGCGCCAGGCGACGCCTTGAACCTGACCTGCGTCAGCATCAGCAGCAACCCC
2110 2120 2130 2140 2150 2160

1720 1730 1740 1750 1760 1770

Hn540-1.Dna CCAGTCAACTTGTCTTGGGACAAGGAAGGAGAGAGGCTGGAAGATGTGGCTGCAAACCC
|||||
Af161715 CCAGTCAACTTGTCTTGGGACAAGGAAGGAGAGAGGCTGGAAGATGTGGCTGCAAACCC
2170 2180 2190 2200 2210 2220

1780 1790 1800 1810 1820 1830

Hn540-1.Dna CAGAGTGCACCGTTCAAAGGCTCCGCTGCATCCAGGAGTGTTTTCTCAGAGTGTCTATCC
|||||
Af161715 CAGAGTGCACCGTTCAAAGGCTCCGCTGCATCCAGGAGTGTTTTCTCAGAGTGTCTATCC
2230 2240 2250 2260 2270 2280

1840 1850 1860 1870 1880 1890

Hn540-1.Dna CGAGACCACGGTCAACGGGTACCTGCCGGGCCCCACAGCGAGGCACTCCGTGAAACCGTG
|||||
Af161715 CGAGACCACGGTCAACGGGTACCTGCCGGGCCCCACAGCGAGGCACTCCGTGAAACCGTG
2290 2300 2310 2320 2330 2340

1900 1910 1920 1930 1940 1950

Hn540-1.Dna AGCTCCTTCTACCGCTTCAATGTGCTGTATCCTCCAGAATTCCTGGGGGAGCAAGTCCGG
|||||
Af161715 AGCTCCTTCTACCGCTTCAATGTGCTGTATCCTCCAGAATTCCTGGGGGAGCAAGTCCGG
2350 2360 2370 2380 2390 2400

1960 1970 1980 1990 2000 2010

Hn540-1.Dna GCAGTGACCGTGGTGGAGCAGGGCCAGGTGCTGCTGCCGGTGTCCGGTGTCCGCTAACCCC
|||||
Af161715 GCAGTGACCGTGGTGGAGCAGGGCCAGGTGCTGCTGCCGGTGTCCGGTGTCCGCTAACCCC
2410 2420 2430 2440 2450 2460

2020 2030 2040 2050 2060 2070

Hn540-1.Dna GCGCCCGAGGCCTTCAACTGGACCTTCCGAGGCTACCGCCTCAGCCAGCTGGGGGTCCC
|||||
Af161715 GCGCCCGAGGCCTTCAACTGGACCTTCCGAGGCTACCGCCTCAGCCAGCTGGGGGTCCC
2470 2480 2490 2500 2510 2520

2080 2090 2100 2110 2120 2130

Hn540-1.Dna CGGCACCGTATCCTGTCTGGAGGGGCTCTGCAGCTGTGGAATGTGACCCGAGCTGACGAT
|||||
Af161715 CGGCACCGTATCCTGTCTGGAGGGGCTCTGCAGCTGTGGAATGTGACCCGAGCTGACGAT
2530 2540 2550 2560 2570 2580

2140 2150 2160 2170 2180 2190

Hn540-1.Dna GGCTTTTATCAGCTGCACTGCCAGAACTCAGAGGGCACCGCTGAGGCGCTGTTGAAGCTG
|||||
Af161715 GGCTTTTATCAGCTGCACTGCCAGAACTCAGAGGGCACCGCTGAGGCGCTGTTGAAGCTG
2590 2600 2610 2620 2630 2640

2200 2210 2220 2230 2240 2250

Hn540-1.Dna GACGTGCATTATGCTCCACCATCCGTGCCCTCCGGGACCCTACTGAGGTGAATGTTGGG
|||||

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      Af161715      GACCCATTATGCTCCCACCATCCGTGCCCTCCGGGACCTACTGAGGTGAATGTTGGG
      2650          2660          2670          2680          2690          2700

Hn540-1.Dna      2260      2270      2280      2290      2300      2310
GGTTCTGTGGACATAGTCTGCACCGTTGACGCCAATCCCATCCTCCCAGAGATGTTTCAGC
|||||
Af161715      GGTTCTGTGGACATAGTCTGCACCGTTGACGCCAATCCCATCCTCCCAGAGATGTTTCAGC
2710      2720      2730      2740      2750      2760

Hn540-1.Dna      2320      2330      2340      2350      2360      2370
TGGGAGAGACTGGGAGAAGAAGAGGAGGATCTGAACCTGGACGACATGGAGAAAGTTTCC
|||||
Af161715      TGGGAGAGACTGGGAGAAGAAGAGGAGGATCTGAACCTGGACGACATGGAGAAAGTTTCC
2770      2780      2790      2800      2810      2820

Hn540-1.Dna      2380      2390      2400      2410      2420      2430
AAGGGATCCACGGGGCGTCTGCGGATTCGCCAAGCCAAGCTATCCCAGGCTGGTGCCTAC
|||||
Af161715      AAGGGATCCACGGGGCGTCTGCGGATTCGCCAAGCCAAGCTATCCCAGGCTGGTGCCTAC
2830      2840      2850      2860      2870      2880

Hn540-1.Dna      2440      2450      2460      2470      2480      2490
CAGTGCATCGTGGACAATGGGGTGGCTCCTGCAGCCAGAGGACTGGTTTCGTCTTGTCGTC
|||||
Af161715      CAGTGCATCGTGGACAATGGGGTGGCTCCTGCAGCCAGAGGACTGGTTTCGTCTTGTCGTC
2890      2900      2910      2920      2930      2940

Hn540-1.Dna      2500      2510      2520      2530      2540      2550
CGATTTGCTCCCCAGGTGGATCAGCCTACTCCCCTAACAAAAGTGGCTGCCGCTGGGGAC
|||||
Af161715      CGATTTGCTCCCCAGGTGGATCAGCCTACTCCCCTAACAAAAGTGGCTGCCGCTGGGGAC
2950      2960      2970      2980      2990      3000

Hn540-1.Dna      2560      2570      2580      2590      2600      2610
AGCACCAGCTCAGCCACACTGCACTGCCGTGCCCGGGGTGTCCCCAACATCGACTTCACT
|||||
Af161715      AGCACCAGCTCAGCCACACTGCACTGCCGTGCCCGGGGTGTCCCCAACATCGACTTCACT
3010      3020      3030      3040      3050      3060

Hn540-1.Dna      2620      2630      2640      2650      2660      2670
TGGACCAAAAACGGGGTCCCTCTGGATCTCCAAGACCCCAGGTACACAGAGCACAGGTAC
|||||
Af161715      TGGACCAAAAACGGGGTCCCTCTGGATCTCCAAGACCCCAGGTACACAGAGCACAGGTAC
3070      3080      3090      3100      3110      3120

      2680      2690      2700      2710      2720      2730

Hn540-1.Dna      CACCAGGGTGTTGTCCACAGCAGCCTCTTGACCATCGCTAATGTGTCTGCGGCCCAGGAC
|||||
Af161715      CACCAGGGTGTTGTCCACAGCAGCCTCTTGACCATCGCTAATGTGTCTGCGGCCCAGGAC
3130      3140      3150      3160      3170      3180

Hn540-1.Dna      2740      2750      2760      2770      2780      2790
TATGCCCTCTTCAAATGCACGGCCACCAATGCCCTTGGCTCTGACCACACCAACATCCAG
|||||
Af161715      TATGCCCTCTTCAAATGCACGGCCACCAATGCCCTTGGCTCTGACCACACCAACATCCAG
3190      3200      3210      3220      3230      3240

Hn540-1.Dna      2800      2810      2820      2830      2840      2850
CTCGTCAGCATCAGCCGCCCTGACCCTCCACTGGGACTGAAGGTTGTCAGCATAAGCCCT
|||||
Af161715      CTCGTCAGCATCAGCCGCCCTGACCCTCCACTGGGACTGAAGGTTGTCAGCATAAGCCCT
3250      3260      3270      3280      3290      3300
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860 2870 2880 2900 2910

Hn540-1.Dna CACTCGGTGGGGCTGGAGTGGGAAGCCTGGCTTTGATGGGGGTCTGCCTCAGAGGTTCCAA
|||||
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3310 3320 3330 3340 3350 3360

2920 2930 2940 2950 2960 2970

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3370 3380 3390 3400 3410 3420

2980 2990 3000 3010 3020 3030

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|||||
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3430 3440 3450 3460 3470 3480

3040 3050 3060 3070 3080 3090

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3490 3500 3510 3520 3530 3540

3100 3110 3120 3130 3140 3150

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|||||
Af161715 ACCCCAGGCCCGACCAGGCTCCTGAAGACACAGACCACCAGCTGCCACAGAGCTGCCT

3550 3560 3570 3580 3590 3600

3160 3170 3180 3190 3200 3210

Hn540-1.Dna CCAGGACCCCCAAGGCTGCCCCTGCTGCCTGTGCTCTTTGCAGTTGGTGGTCTTCTGCTG
|||||
Af161715 CCAGGACCCCCAAGGCTGCCCCTGCTGCCTGTGCTCTTTGCAGTTGGTGGTCTTCTGCTG

3610 3620 3630 3640 3650 3660

3220 3230 3240 3250 3260 3270

Hn540-1.Dna CTCTCCAATGCCTCCTGTGTTGGGGGTCTCCTCTGGCGGAGAAGACTGAGGCGCCTTGCT
|||||
Af161715 CTCTCCAATGCCTCCTGTGTTGGGGGTCTCCTCTGGCGGAGAAGACTGAGGCGCCTTGCT

3670 3680 3690 3700 3710 3720

3280 3290 3300 3310 3320 3330

Hn540-1.Dna GAGGAGATCTCAGAGAAGACAGAGGCAGGGTCGGAGGACAGGATCAGGAATGAATATGAG
|||||
Af161715 GAGGAGATCTCAGAGAAGACAGAGGCAGGGTCGGAGGACAGGATCAGGAATGAATATGAG

3730 3740 3750 3760 3770 3780

3340 3350 3360 3370 3380 3390

Hn540-1.Dna GAGAGTCAGTGGACTGGGGACCGGGACACGAGAAGCTCCACGGTTAGCACAGCAGAAGTG
|||||
Af161715 GAGAGTCAGTGGACTGGGGACCGGGACACGAGAAGCTCCACGGTTAGCACAGCAGAAGTG

3790 3800 3810 3820 3830 3840

3400 3410 3420 3430 3440 3450

Hn540-1.Dna GACCCAAATTACTACTCCATGAGGGACTTCAGCCCCAGCTTCCCCAACACTGGAGGAG
|||||
Af161715 GACCCAAATTACTACTCCATGAGGGACTTCAGCCCCAGCTTCCCCAACACTGGAGGAG

3850 3860 3870 3880 3890 3900

3460 3470 3480 3490 3500 3510

Hn540-1.Dna GTGCTGTATCACCAAGGTGCTGAAGGCGAGGACATGGCCTTCCCCGGACACCTGCATGAT
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      Af161715      GTGCTATACCAAGGTGCTGAAGGCGAGGACATGCTTCCCCGGACACCTGCATGAT
      3910          3920          3930          3940          3950          3960

Hn540-1.Dna      3520          3530          3540          3550          3560          3570
      GAAGTGGAGAGAGCCTATGGCCCGCCTGGGGCCTGGGGACCCCTCTATGATGAAGTACGA
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Af161715      3970          3980          3990          4000          4010          4020
      GAAGTGGAGAGAGCCTATGGCCCGCCTGGGGCCTGGGGACCCCTCTATGATGAAGTACGA

Hn540-1.Dna      3580          3590          3600          3610          3620          3630
      ATGGACCCCTATGACCTTCGCTGGCCTGAGGTCCAATGTGAGGATCCGAGGGGAATCTAC
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Af161715      4030          4040          4050          4060          4070          4080
      ATGGACCCCTATGACCTTCGCTGGCCTGAGGTCCAATGTGAGGATCCGAGGGGAATCTAC

Hn540-1.Dna      3640          3650          3660          3670          3680          3690
      AACCAGGTGGCAGCAGACATGGATGCTGTGGAAGCTAGCTCTCTGCCGTTTGAGCTGAGG
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Af161715      4090          4100          4110          4120          4130          4140
      GACCAGGTGGCAGCAGACATGGATGCTGTGGAAGCTAGCTCTCTGCCGTTTGAGCTGAGG

Hn540-1.Dna      3700
      GGACATCTGGTGTGA
      |||||||||||||||

Af161715      4150          4160          4170          4180          4190          4200
      GGACATCTGGTGTGAGACGCTTCACAACACCCGTTTCCTACAGCCCTGGAGAAGATGTGA

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Hn540-1.Dna
Emrod:Af168466

ID AF168466 standard; RNA; ROD; 3729 BP.

AC AF168466;
SV AF168466.1
DT 21-OCT-1999 (Rel. 61, Created)
DT 21-OCT-1999 (Rel. 61, Last updated, Version 1)
DE Mus musculus nephrin (Nphs1) mRNA, complete cds.
KW .
OS Mus musculus (house mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP 1-3729
RX MEDLINE; 99436348.
RA Holzman L.B., St John P.L., Kovari I.A., Verma R., Holthofer H.,
RA Abrahamson D.R.;
RT "Nephrin localizes to the slit pore of the glomerular epithelial cell";
RL Kidney Int. 56(4):1481-1491(1999).
RN [2]
RP 1-3729

RA Holzman L.B., St John P.L., Kovari I.A., Verma R., Holthofer H.,
RA Abrahamson D.R.;
RT ;
RL Submitted (12-JUL-1999) to the EMBL/GenBank/DDBJ databases.
RL Internal Medicine/Nephrology, University of Michigan Medical School, 1560
RL MSRB II, P.O. Box 0676, Ann Arbor, MI 48109-0676, USA
DR SPTREMBL; Q9QZS7; Q9QZS7.
FH Key Location/Qualifiers
FH
FT source 1. 3729
FT /db_xref="taxon:10090"
FT /organism="Mus musculus"
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Emhum1:Af035835

ID AF035835 standard; RNA; HUM; 4285 BP.

AC AF035835;

SV AF035835.1

DT 08-APR-1998 (Rel. 55, Created)

DT 03-MAR-2000 (Rel. 62, Last updated, Version 3)

DE Homo sapiens nephrin (NPHS1) mRNA, complete cds.

KW .

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP 1-4285

RX MEDLINE; 98325371.

RA Kestila M., Lenkkeri U., Mannikko M., Lamerdin J., McCready P., Putaala H.,

RA Ruotsalainen V., Morita T., Nissinen M., Herva R., Kashtan C.E.,

RA Peltonen L., Holmberg C., Olsen A., Tryggvason K.;

RT "Positionally cloned gene for a novel glomerular protein--nephrin--is

RT mutated in congenital nephrotic syndrome";

RL Mol. Cell 1(4):575-582(1998).

RN [2]

RP 1-4285

RA Lenkkeri U., Kestila M., Mannikko M., Lamerdin J., McCready p., Putaala H.,

RA Ruotsalainen V., Morita T., Nissinen M., Herva R., Kashtan C.E.,

RA Peltonen L., Holmberg C., Olsen A., Tryggvason K.;

RT ;

RL Submitted (26-NOV-1997) to the EMBL/GenBank/DDBJ databases.

RL Biochemistry, University of Oulu, Linnanmaa, Oulu 90570, Finland

DR SPTREMBL; O60500; O60500.

FH Key Location/Qualifiers

FH

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SCORES Init1: 11557 Initn: 12214 Opt: 12066 z-score: 17125.7 E(): 0
83.1% identity in 3474 bp overlap

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                                10      20      30      40
Hn540-1.Dna      ATGTCCAGTTTGA TCTCCCTGCTGCTCATGGGAATGCTGACCTCAGGC
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Af035835      ATGGCCCTGGGGACGACGCTCAGGGCTTCTCTCCTGCTCCTGGGGCTGCTGACTGAAGGC
                   10      20      30      40      50      60

                                50      60      70      80      90      100
Hn540-1.Dna      CTGGCCGAGTCGCCAGTCCCCACCTCAGCACCTCGAGGCTTCTGGGCTCTGTCTGAAAAC
                   | | | | | | | | | | | | | | | | | | | | | |
Af035835      CTGGCGCAGTTGGCGATTCTGCTCCGTTCCCCGGGGCTTCTGGGCCCTGCCTGAAAAC
                   70      80      90      100      110      120

                                110      120      130      140      150      160
Hn540-1.Dna      CTGACTGCGGTGGAAGGGACAACAGTTAAGCTATGGTGCGGTGTCAGGGCCCCCTGGCAGT
                   | | | | | | | | | | | | | | | | | | | | | |
Af035835      CTGACGGTGGTGGAGGGGGCCTCAGTGGAGCTGCGTTGTGGGGTCAGCACCCCTGGCAGT
                   130      140      150      160      170      180

                                170      180      190      200      210      220
Hn540-1.Dna      GTGGTGCACTGGGCTAAGGATGGGCTGCTTCTGGGTCCAAACCCGAAGATGCCAGGCTTC
                   | | | | | | | | | | | | | | | | | | | | | |
Af035835      GCGGTGCAATGGGCCAAAGATGGGCTGCTCCTGGGCCCCGACCCAGGATCCCAGGCTTC
                   190      200      210      220      230      240

                                230      240      250      260      270      280
Hn540-1.Dna      CCGAGGTACAGCCTGGAAGGAGATCGTGCTAAAGGCGAGTTCACCTGCTTATTGAAGCC
                   | | | | | | | | | | | | | | | | | | | | | |
Af035835      CCGAGGTACCGCCTGGAAGGGGACCCTGCTAGAGGTGAATTCCACCTGCACATCGAGGCC
                   250      260      270      280      290      300

                                290      300      310      320      330      340
Hn540-1.Dna      TGTGACCTCAGTGATGACGCAGAGTATGAATGCCAAGTCGGCCGCTCAGAGTTGGGTCCC
                   | | | | | | | | | | | | | | | | | | | | | |
Af035835      TGTGACCTCAGCGATGACGCGGAGTATGAGTGCCAGGTTCGGCCGCTCTGAGATGGGGCCC
                   310      320      330      340      350      360

                                350      360      370      380      390      400
Hn540-1.Dna      GAGCTTGTGTCTCCTAAAGTAATCCTCTCCATTCTAGTTTCCCCAAGGTGCTTCTGTTG
                   | | | | | | | | | | | | | | | | | | | | | |
Af035835      GAGCTCGTGTCTCCAGAGTGATCCTCTCCATCCTGTTCTCCCAAGCTGCTCCTGCTG
                   370      380      390      400      410      420

                                410      420      430      440      450      460
Hn540-1.Dna      ACCCCCGAGGCAGGAAGCACAGTGACCTGGGTAGCTGGGCAGGAGTATGTGGTCACCTGT
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Af035835      ACCCCAGAGGCAGGCACCATGGTCACTGGGTAGCTGGGCAGGAGTACGTGGTCAACTGT
                   430      440      450      460      470      480

                                470      480      490      500      510      520
Hn540-1.Dna      GTGTCTGGGGATGCAAACAGCACCTGACATCACCTTCATCCAGAGTGGACGAACATA
                   | | | | | | | | | | | | | | | | | | | | | |
Af035835      GTGTCTGGGGACGCGAAGCCAGCACCTGACATCACCATTCCTGAGTGGACAGACAATA
                   490      500      510      520      530      540

                                530      540      550      560      570      580
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Page -27-

Page -28-

Page -29-

Page -30-

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ID      Z25338 standard; cDNA; 4285 BP.
AC      Z25338;
DT      17-DEC-1999 (first entry)
DE      Human nephrin nucleotide sequence.
KW      Human; nephrin; NPHS1 gene; basement membrane disease; proteinuria;
KW      nephrotic syndrome; kidney disease; diagnosis; clinical nephrology;
KW      glomerular filtration barrier; glomerulonephritis; ss.
OS      Homo sapiens.
FH      Key                      Location/Qualifiers
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FT                                  /note= "putative signal peptide"
FT      mat peptide              67. .3723
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FT                               /*tag= d
FT                               /note= "deletion mutation FIN-Major"
FT   misc_feature 3800..3804
FT                               /*tag= e
FT                               /note= "nonsense mutation in exon 26 FIN-Major"
FT   misc_feature 3178..3258
FT                               /*tag= f
FT                               /note= "putative transmembrane domain"
PN   WO9947562-A1.
PD   23-SEP-1999.
PF   16-MAR-1999; U05578.
PR   18-MAR-1998; US-040774.

PA   (BIOS-) BIOSTRATUM INC.
PI   Tryggvason K, Kestila M, Lenkkeri U, Mannikko M;
DR   WPI; 1999-590967/50.
DR   P-PSDB; Y42167.
PT   New isolated nucleic acid (gene) encoding nephrin useful in methods for
PT   screening for susceptibility to basement membrane disease -
PS   Claim 1; Page 34-42; 60pp; English.
CC   The present sequence represents the NPHS1 gene which encodes nephrin.
CC   The present invention describes methods for the treatment of an
CC   individual with basement membrane disease by administration of the
CC   nephrin protein, as well as methods of gene therapy using therapeutic
CC   nucleic acid constructs containing an expressible nucleic acid with

CC   the NPHS1 sequence. NPHS1 appears to solely affect the kidney and
CC   therefore provides a unique model for studies on the glomerular
CC   filtration barrier. Abnormal function of the filtration barrier is a
CC   major complication in many clinically important kidney diseases such as
CC   nephrotic syndromes and glomerulonephritides and therefore this
CC   invention will help in the understanding of clinical nephrology.
CC   The identification of the NPHS1 gene immediately finds applications
CC   for diagnosis of the disease.
SQ   Sequence 4285 BP; 886 A; 1294 C; 1302 G; 803 T; . . .

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SCORES Init1: 11557 Initn: 12214 Opt: 12066 z-score: 17125.7 E(): 0

83.1% identity in 3474 bp overlap

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                        10      20      30      40
Hn540-1.Dna      ATGTCCAGTTTGACTCCCCTGCTGCTCATGGGAATGCTGACCTCAGGC
                  | | | | | | | | | | | | | | | | | |
Z25338      ATGGCCCTGGGGACGACGCTCAGGGCTTCTCTCCTGCTCCTGGGGCTGCTGACTGAAGGC
                  10      20      30      40      50      60

                        50      60      70      80      90      100
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                  | | | | | | | | | | | | | | | | | | | | | |
Z25338      CTGGCGCAGTTGGCGATTCTGCCTCCGTTCCCGGGGCTTCTGGGCCCTGCCTGAAAAC
                  70      80      90      100      110      120

                        110      120      130      140      150      160
Hn540-1.Dna      CTGACTGCGGTGGAAGGGACAACAGTTAAGCTATGGTGCGGTGTGAGGGCCCCCTGGCAGT
                  | | | | | | | | | | | | | | | | | | | | | |
Z25338      CTGACGGTGGTGGAGGGGGCCTCAGTGGAGCTGCGTTGTGGGGTCAGCACCCCTGGCAGT
                  130      140      150      160      170      180

                        170      180      190      200      210      220
Hn540-1.Dna      GTGGTGCAGTGGGCTAAGGATGGGCTGCTTCTGGGTCCAAACCCGAAGATGCCAGGCTTC
                  | | | | | | | | | | | | | | | | | | | | | |
Z25338      GCGGTGCAATGGGCCAAAGATGGGCTGCTCCTGGGCCCGACCCAGGATCCCAGGCTTC
                  190      200      210      220      230      240

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Page -33-

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910 920 930 940 950 960

Hn540-1.Dna 950 960 970 980 990 1000
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|||||
Z25338 AACAGCGTGTCTGCAGGGACCCAGGAGCACGGCATCACACTGCAGGTACCTTTCCCCCT
970 980 990 1000 1010 1020

Hn540-1.Dna 1010 1020 1030 1040 1050 1060
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|||
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1090 1100 1110 1120 1130 1140

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1210 1220 1230 1240 1250 1260

Hn540-1.Dna 1250 1260 1270 1280 1290 1300
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1270 1280 1290 1300 1310 1320

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1450 1460 1470 1480 1490 1500

Page -35-

2110 2120 2130 2140 2150 2160

Hn540-1.Dna 2150 2160 2170 2180 2190 2200
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2410 2420 2430 2440 2450 2460

2450 2460 2470 2480 2490 2500

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2590 2600 2610 2620 2630 2640

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2710 2720 2730 2740 2750 2760

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